

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 21, 2003, 17:55:24 ; Search time 20 seconds

(without alignments)
389.877 Million cell updates/sec

Title: US-09-527-376-2

Perfect score: 981

Sequence: 1 MTAPSCAFFPQFRQPSVSL.....SPVGMIPDIYEKEVRLMPL 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	511	52.1	198	1 DUSE_HUMAN	O95147 homo sapien
2	500	51.0	198	1 DUSE_MOUSE	Q911y7 mus musculu
3	252	25.7	367	1 DUS1_HUMAN	P28562 homo sapien
4	252	25.7	367	1 DUS1_MOUSE	P28563 mus musculu
5	252	25.7	367	1 DUS1_RAT	Q64623 rattus norv
6	238	24.3	394	1 DUS4_HUMAN	Q13115 homo sapien
7	236	24.1	375	1 DUS4_CHICK	Q9PW71 gallus gail
8	236	24.1	395	1 DUS4_RAT	Q62767 rattus norv
9	233	23.8	619	1 VRP1_CAEEL	Q10038 caenorhabdi
10	230	23.4	235	1 DUSF_HUMAN	Q9HLR2 homo sapien
11	221	22.5	384	1 DUS5_HUMAN	Q16690 homo sapien
12	219.5	22.4	384	1 DUS5_RAT	Q54838 rattus norv
13	219.5	22.4	625	1 DUS8_HUMAN	Q13202 homo sapien
14	212.5	21.7	563	1 DUS8_MOUSE	Q09112 mus musculu
15	208.5	21.3	565	1 DUSX_HUMAN	Q9BY84 homo sapien
16	208	21.2	318	1 DUS2_MOUSE	Q05922 mus musculu
17	200	20.4	482	1 DUS4_HUMAN	Q9Y6W6 homo sapien
18	197	20.1	314	1 DUS2_HUMAN	Q05923 homo sapien
19	194.5	19.8	198	1 DUS7_HUMAN	Q9UL16 homo sapien
20	183.5	18.7	280	1 DUS7_RAT	Q63340 rattus norv
21	183.5	18.7	320	1 DUS7_MOUSE	Q16829 homo sapien
22	183.5	18.7	320	1 DUS7_MOUSE	Q91246 mus musculu
23	181.5	18.5	198	1 DUSD_MOUSE	Q9QYJ7 mus musculu
24	180.5	18.4	384	1 DUS9_HUMAN	Q95956 homo sapien
25	174	17.7	381	1 DUS6_HUMAN	Q16828 homo sapien
26	174	17.7	381	1 DUS6_MOUSE	Q9DBB1 mus musculu
27	174	17.7	381	1 DUS6_RAT	Q64346 rattus norv
28	165.5	16.9	292	1 Y042_CAEEL	P34680 caenorhabdi
29	162.5	16.6	185	1 DUS3_HUMAN	P51452 homo sapien
30	160	16.3	209	1 Y1L3_YEAST	P04799 saccharomyc
31	159.5	16.3	185	1 DUS3_MOUSE	Q947X3 mus musculu
32	155	15.8	489	1 MSG5_YEAST	P38590 saccharomyc
33	151	15.4	171	1 VHO1_RACVI	P80994 raccoon pox

ALIGNMENTS

RESULT 1

ID	DUSE_HUMAN	STANDARD;	PRT;	198 AA.
AC	O95147;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Dual specificity protein phosphatase 14 (EC 3.1.3.48) (EC 3.1.3.16)			
DE	(Mitogen-activated protein kinase phosphatase 6) (MAP kinase phosphatase 6) (MKP-6) (MKP-1 like protein tyrosine phosphatase) (MKP-L).			
DE	DUSP14 OR MKP6.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yuan Y., Suphapeetiporn K., Sun H.;			
RT	"MKP-L, a novel MKP-1 like protein tyrosine phosphatase.";			
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=20571897; PubMed=11123293;			
RA	Marti F., Krause A., Post N.H., Lyddane C., Dupont B., Sadelain M., King P.D.;			
RT	"Negative-feedback regulation of CD28 costimulation by a novel mitogen-activated protein kinase phosphatase, MKP6.";			
RL	J. Immunol. 166:197-206(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Strassberg R.;			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
CC	!- FUNCTION: Involved in the inactivation of MAP kinases. Dephosphorylates ERK, JNK and p38 MAP-kinases.			
CC	!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.			
CC	!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.			
CC	!- SUBUNIT: Intercats with CD28.			
CC	!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; AF038844; AAD02105.1; -			
DR	EMBL; AF120032; AAF28861.1; -			
DR	EMBL; BC000370; AAH00370.1; -			
DR	EMBL; BC001894; AAH01894.1; -			

P20495 vaccinia vi
P07239 vaccinia vi
P33064 variola vir
Q9uni6 homo sapien
Q39491 chlamydomon
P38148 saccharomyc
Q05297 myxoma viru
Q02256 saccharomyc
Q91592 fowlpox vir
P43078 candida alb
O10273 oryza pseu
P76093 escherichia

34 147 15.0 171 1 DUSP_VACCC
35 147 15.0 171 1 DUSP_VACCC
36 144 14.7 171 1 DUSP_VARV
37 141 14.4 340 1 DUSC_HUMAN
38 139.5 14.2 276 1 PTP3_CHLEU
39 137 14.0 807 1 YB9T_YEAST
40 120.5 12.3 178 1 DUSP_MTXVL
41 117 11.9 364 1 PVH1_YEAST
42 107 10.9 166 1 DUSP_FOPVP
43 107 10.9 597 1 PTPX_CANAL
44 99 10.1 160 1 PTP2_NPVOP
45 93 9.5 430 1 YNBD_ECOLI

DR EMBL: BC004448; AA04448.1; --
 DR HSP: Q16828; IMRP.
 DR Genew: HGNC:17007; DUSP14.
 DR MIM: 606618; --
 DR InterPro: IPR000340; DS_phosphatase.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR Pfam: PF00782; DSPC; 1.
 DR SMART: SM00195; DSPC; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00556; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW DOMAIN.
 FT ACT_SITE 111 131 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 111 131 BY SIMILARITY.
 SQ SEQUENCE 198 AA; 22255 MW; 6AFAELB3A24F9AA CRC64;
 Query Match 52.1%; Score 511; DB 1; Length 198;
 Best Local Similarity 50.3%; Pred. No. 6.9e-44;
 Matches 90; Conservative 40; Mismatches 49; Indels 0; Gaps 0;
 QY 9 PVQFPQPSVGLSQTISLYISNGVAANKMLSSNOITWVNSVEVVTLYEDIQYMQ 68
 DB 16 PMWISGDDGGIAQITSSFLGSGVASNRHLLQAGITCVNATIEIPNFWPOPEYVK 75
 QY 69 VPVADSPNSRLCDFDPIADHSHVEMKGRILLHCAAGVSRAALCLAYLMKYRAMSL 128
 DB 76 VPLADPHAPIGLYETVADKIESVSRKHGATLVHCAAGVSRAALCLAYLMKYRAMSL 135
 QY 129 DAHTWTKSCRTPIRNSGFWEOILHYEFOLFGKNTVMYSSPVGMIPDIYEKRLMIP 187
 DB 136 EAYNVKARPVIRPNVGFWRQLIDYEROLFGRSTVKVQVTPYGIYVDPVYKESRHLMP 194
 RESULT 2
 DUSE_MOUSE
 ID DUSE_MOUSE STANDARD; PRT; 198 AA.
 AC Q9JLY7; Q9D715;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Dual specificity protein phosphatase 14 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Mitogen-activated protein kinase phosphatase 6) (MAP kinase phosphatase 6) (MKP-6).
 GN DUSP14 OR MKP6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=20371897; PubMed=11123293;
 RA Marti F., Krause A., Post N.H., Lyddane C., Dupont B., Sadelain M., King P.D.;
 RT "Negative-feedback regulation of CD28 costimulation by a novel mitogen-activated protein kinase phosphatase, MKP6.";
 RL J. Immunol. 166:197-206(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz T., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;
 "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAUSBERG R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Involved in the inactivation of MAP kinases.
 CC Dephosphorylates ERK, JNK and p38 MAP-kinases.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
 CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: AF120113; AAF28862.1; --
 DR EMBL: AK009744; BAB26474.1; --
 DR EMBL: BC002130; AA02130.1; --
 DR HSSP: Q16828; IMRP.
 DR MGD: MGI:1927168; Dusp14.
 DR InterPro: IPR000340; DS_phosphatase.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR Pfam: PF00782; DSPC; 1.
 DR SMART: SM00195; DSPC; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00556; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase.
 FT ACT_SITE 91 156 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 111 131 BY SIMILARITY.
 FT CONFLICT 38 38 R -> K (IN REF. 1).
 FT CONFLICT 150 150 P -> H (IN REF. 1).
 FT CONFLICT 160 160 D -> E (IN REF. 1).
 FT CONFLICT 163 163 S -> R (IN REF. 1).
 SQ SEQUENCE 198 AA; 22311 MW; 5C2B4210E886DFCF CRC64;
 Query Match 51.0%; Score 500; DB 1; Length 198;
 Best Local Similarity 50.8%; Pred. No. 8.7e-43;
 Matches 91; Conservative 37; Mismatches 51; Indels 0; Gaps 0;
 QY 9 PVQFPQPSVGLSQTISLYISNGVAANKMLSSNQITWVNSVEVVTLYEDIQYMQ 68
 DB 16 PMWISGDDGGIAQITSSFLGSGVASNRHLLQAGITCVNATIEIPNFWPOPEYVK 75
 QY 69 VPVADSPNSRLCDFDPIADHSHVEMKGRILLHCAAGVSRAALCLAYLMKYRAMSL 128
 DB 76 VPLADPHAPIRLYETVADKIESVSRKHGATLVHCAAGVSRAALCLAYLMKYRAMSL 135
 QY 129 DAHTWTKSCRTPIRNSGFWEOILHYEFOLFGKNTVMYSSPVGMIPDIYEKRLMIP 187
 DB 136 EAYNVKARPVIRPNVGFWRQLIDYEROLFGRSTVKVQVTPYGIYVDPVYKESRHLMP 194
 RESULT 3
 DUSL_HUMAN
 ID DUSL_HUMAN STANDARD; PRT; 367 AA.
 AC P28562;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)


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DR Pfam: PF00581; Rhodanese; 1.
DR Pfam: PF00782; DSEPC; 1.
DR SMART: SM00195; DSEPC; 1.
DR SMART: SM00450; RHOD; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS0034; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase; Cell cycle.
FT DOMAIN 9 135 RHODANESE.
FT DOMAIN 175 367 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 258 258
FT MUTAGEN 258 258 C->S: LOSS OF ACTIVITY.
FT SEQUENCE 367 AA; 39369 MW; 50B5F90FEBBD19AB CRC64;
Query Match 25.7%; Score 252; DB 1; Length 367;
Best Local Similarity 34.3%; Pred. No. 1.1e-17;
Matches 59; Conservative 29; Mismatches 80; Indels 4; Gaps 1;
QY 5 SCAPPVQFRPSVGLSQITKSLYSINGVAANNKLSSNQITWVINSVVEVNTLYEDI 64
DB 163 SCSTPLY----DOGGPVEILSLFLGSAYHASKRMDLDALGITALINVSANCPNHFEGHY 218
QY 65 QYMGVPVADSPNSRLCDFFDPDIADHIHSVEMKQGTLLHCAAGVSRSAAALCLAYLMKYHA 124
DB 219 QYKSIPVEDNHKADISSWENEAIDFDSIKDAGGRVVFHCAGISRSATICLAYLMRTNR 278
QY 125 MSLLDAHTWTKSCRPIIRNSGIWEQLIHFEQLFGKNTVHWVSPVGMIPD 176
DB 279 VKLDAEFYKQRKSIISPNFSGMLQLQFESQVLAIPHCSAAGSPAMAVLD 330
RESULT 5
DUSL_RAT STANDARD; PRT; 367 AA.
ID AC Q04623;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dual specificity protein phosphatase 1 (EC 3.1.3.48) (EC 3.1.3.16)
DE (NAP kinase phosphatase-1) (MKP-1) (Protein-tyrosine phosphatase
DE CL100).
GN DUSPL OR CL100.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lung;
RA Mada M., Schlegel W., Arkinstall S.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP
CC KINASE ERK2 ON BOTH THR-183 AND TYR-185.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC -----
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CC -----
CC EMBL; X84004; CAA58828.1; -.
CC HSP; Q16828; IMKP.
CC InterPro; IPR000340; DR
CC InterPro; IPR001763; Rhodanese-like.
CC DR

```


RA Misra-Press A., Rim C.S., Yao E., Roberson M.S., Stork P.J.S.;
 RT "A novel mitogen-activated protein kinase phosphatase. Structure,
 expression, and regulation.";
 RL J. Biol. Chem. 270:14587-14596(1995).
 CC -|- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
 CC DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
 CC ERK1 AND ERK2 (BY SIMILARITY).
 CC -|- CATALYTIC ACTIVITY: protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -|- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -|- TISSUE SPECIFICITY: EXPRESSED AT MODERATE LEVELS IN NEARLY ALL
 CC TISSUES AND CELLS INCLUDING BRAIN, SPLEEN, AND TESTES WITH THE
 CC HIGHER EXPRESSION IN THE HEART AND LUNG AND LOWER EXPRESSION IN
 CC SKELETAL MUSCLE AND KIDNEY. UNDETECTABLE IN LIVER. EXPRESSED IN
 CC MANY AREAS OF THE BRAIN WITH VERY STRONG EXPRESSION IN THE
 CC HIPPOCAMPUS, PIRIFORM CORTEX, AND THE SUPRACHIASMATIC NUCLEUS.
 CC -|- INDUCTION: BY MITOGENS AND BY STRESS.
 CC -|- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -|- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
 CC
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 CC
 CC EMBL: U23438; AAC52493.1; -;
 CC HSSP: Q16828; LMKP.
 CC InterPro: IPR000340; DS_phosphatase.
 CC InterPro: IPR001763; Rhodanese-like.
 CC InterPro: IPR000387; TYR_phosphatase.
 CC Pfam: PF00581; Rhodanese; 1.
 CC Pfam: PF00782; DSPC; 1.
 CC SMART: SM00195; DSPC; 1.
 CC SMART: SM00450; RHOD; 1.
 CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 CC PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
 CC Hydrolase; Nuclear protein.
 CC FT DOMAIN 34 158 RHODANESE.
 CC FT DOMAIN 198 395 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 281 BY SIMILARITY.
 CC SQ SEQUENCE 395 AA: 43187 MW: A90EFD378A050FD CRC64:
 Query Match 24.1%; Score 236; DB 1; Length 395;
 Best Local Similarity 33.9%; Pred. No. 4.6e-16;
 Matches 57; Conservative 30; Mismatches 77; Indels 4; Gaps 1;
 QY 5 SCAPPVQFRPSVSGLSQITKSLYISNGVAANKMLSSNQITMIVNSVEVNTLYEDI 64
 DB 186 SCGTPLH----DQGGVEILPFLYLGSAVHAARDLDALGATALLNVSDCPNHPG 241
 QY 65 QYQVQVADSPNRLCDFDPIADHSHVEMKGRITLLHCAAGVSSAALCLAYLAKYHA 124
 DB 242 QYKICPEVDNHRKADISSWEAELEYIDAVDCRGVILVHCQAGISRSATICLAYLAKKR 301
 QY 125 MSLLDHTTKSCRPPIRPSNGFWEQLIHYEFQFGKNTVHVYSSPVG 172
 DB 302 VRLAEAFEVKQRRIISNFSFMGQLQFESQVLTSCAAEAASPSG 349
 RESULT 9
 ID VHP1_CAEEL STANDARD; PRT; 619 AA.
 AC Q10038;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Protein-tyrosine phosphatase vhp-1 (EC 3.1.3.48).
 GN VHP-1 OR F08B1.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Chissao S.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -|- CATALYTIC ACTIVITY: protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -|- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC
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 CC
 CC EMBL: U23178; AAC46719.1; -;
 CC HSSP: Q16828; LMKP.
 CC WormPep: F08B1.1; CE01899.
 CC InterPro: IPR000340; DS_phosphatase.
 CC InterPro: IPR000387; TYR_phosphatase.
 CC Pfam: PF00782; DSPC; 1.
 CC SMART: SM00195; DSPC; 1.
 CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 CC PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
 CC Hydrolase.
 CC FT DOMAIN 200 269 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT DOMAIN 92 95 POLY-SER.
 CC FT DOMAIN 351 354 POLY-SER.
 CC FT DOMAIN 455 472 POLY-SER.
 CC FT DOMAIN 483 488 POLY-SER.
 CC FT ACT_SITE 224 224 BY SIMILARITY.
 CC SQ SEQUENCE 619 AA: 66354 MW: 369E326F615D0529 CRC64:
 Query Match 23.8%; Score 233; DB 1; Length 619;
 Best Local Similarity 33.3%; Pred. No. 1.6e-15;
 Matches 48; Conservative 35; Mismatches 59; Indels 2; Gaps 1;
 QY 14 QPSVSGLSQITKSLYISNGVAANKMLSSNQITMIVNSVEVNT--LYEDIQWQV 71
 DB 132 OPTGDTITLTNTNIVLGSOISLDETMLDALDISVIVNLSMTCKPSVCIKEDKNEFIPV 191
 QY 72 ADSPNSRLCDFDPIADHSHVEMKGRITLLHCAAGVSSAALCLAYLAKYHAMSLLDAH 131
 DB 192 NDSYQEKSPYFPMPAYEFLEKCRAGKCLIEHLAGISRPTAISYIMRYKMGSDDAY 251
 QY 132 TWTKSCRPPIRPSNGFWEQLIHYE 155
 DB 252 RYVKERRPSISPNFPMGOLLEVE 275
 RESULT 10
 ID DUSEF_HUMAN STANDARD; PRT; 235 AA.
 AC Q9H1R2;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 15 (EC 3.1.3.48) (EC 3.1.3.16).
 GN DUSP15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

```

[1]
SEQUENCE FROM N.A.
RP MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggus J.C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.B., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hunkle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharshaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnell L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Pratchinalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symcote N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20. ";
RL Nature 414:865-871(2001).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
-----
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-----
EMBL: AL160175; CAC10008.2; ALT_SEQ.
DR HSP; P51452; 1VHR.
DR Genes; HNC16236; DUSP15.
DR InterPro; IPR000340; DS_Phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50034; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase.
FT DOMAIN 65 133 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 88 88 BY SIMILARITY.
SQ SEQUENCE 235 AA; 26152 MW; A3AF26789834FECB CRC64;
Query Match 23.4%; Score 230; DB 1; Length 235;
Best Local Similarity 31.4%; Pred. No. 9.5e-16;
Matches 55; Conservative 34; Mismatches 76; Indels 10; Gaps 3;
QY 18 SGLSQITKSLYSINGVAANKKMLSSNOITMIVNSVEVNTYFEDIQYQVFPVADSPNS 77
Db 3 NGMTKVLPLGLYLGNFIDAKOLDKLDGRNKKTHIISIH-ESPQFLQIDITYLRIPVADTPEV 61
QY 78 RLCDFFPIADHHSVEMKOGRTLLHCAAGVSRSAALCLAYLAKYHMSLLDAHTWTKSC 137
Db 62 PIKHFKECINFTHCCRLNGCNCILVHCAGLSRSTTTTITAYTMTVTLGWRDVLAEIKAT 121
QY 138 RPIRPNASGFWEOILHYEFQLFG----KNTVHMVSSPGMIPDITKEVRLKIPL 188

```

FT DOMAIN 7 139 RHODANESE.
 FT DOMAIN 180 384 PROTEIN-TYROSINE PHOSPHATASE
 FT DOMAIN 53 74 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT ACT_SITE 263 82 POLY-GLY.
 FT ACT_SITE 263 82 BY SIMILARITY.
 FT CONFLICT 9 11 RGL -> GHV (IN REF. 2).
 FT CONFLICT 71 71 A -> R (IN REF. 2).
 FT CONFLICT 105 106 AR -> F (IN REF. 2).
 SQ SEQUENCE 384 AA; 42107 MW; D2B726F7C0414306 CRC64;

 Query Match 22.5%; Score 221; DB 1; Length 384;
 Best Local Similarity 34.3%; Pred. No. 1.4e-14;
 Matches 48; Conservative 24; Mismatches 58; Indels 0; Gaps 0;

 QY 19 GLSQITKSLYISNGVAANKMLSSNQITWVINSVEVYNTLYEDIQYMQVPVADSPNSR 78
 DB 178 GPVEILPFLYLGSAHAKCEFLANLHITALLNVSRRTSEACTTHLYKWIPIVEDSHAD 237

 QY 79 LCDFFDPIADHITHSVEMKQRTLLHCAAGVSRSAALCLAYLMKYHAMSLLDHATWTKSCR 138
 DB 238 ISSHFOEAIDFIDCVREKGGKVLVHCEAGVSRSPICMAYLMKTKOFLRKEAPDYIKORR 297

 QY 139 PIIRPNSGFWEQLIHYEFOL 158
 DB 298 SMVSPNFGFMGQLQYSEI 317

 RESULT 12
 DUS5_RAT STANDARD; PRT: 384 AA.
 AC 054836;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE Dual specificity protein phosphatase 5 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (MAP-kinase phosphatase CPG21).
 GN DUSP5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WiStar;
 RX MEDLINE=98364306; PubMed=9699150;
 RA Havroni D., Ratner A., Bundman M., Lederfein D., Gabarrah A.,
 RA Mangelus M., Silverman M.A., Kedar H., Naor C., Kornuc M., Hanoch T.,
 RA Seger R., Inell L.E., Nedivi E., Richter-Levin G., Citri Y.;
 RT "Hippocampal plasticity involves extensive gene induction and multiple
 cellular mechanisms";
 RL J. Mol. Neurosci. 10:75-98(1998).
 CC -!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
 CC PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
 CC SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
 CC -----
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 CC -----
 CC EMBL: AF013144; AAB94858.1;
 CC HSP; Q16828; IMKP.

DR InterPro: IPR000340; DS_phosphatase.
 DR InterPro: IPR001763; Rhodanese-like.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR Pfam: PF00581; Rhodanese; 1.
 DR Pfam: PF00783; DSPC; 1.
 DR SMART: SM00195; DSPC; 1.
 DR SMART: SM00450; RHOD; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS00054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase; Nuclear protein.
 FT DOMAIN 7 139 RHODANESE.
 FT DOMAIN 180 384 PROTEIN-TYROSINE PHOSPHATASE.
 FT DOMAIN 53 74 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 79 82 POLY-GLY.
 FT ACT_SITE 263 82 BY SIMILARITY.
 SQ SEQUENCE 384 AA; 42094 MW; 5644059B8D348700 CRC64;

 Query Match 22.4%; Score 219.5; DB 1; Length 384;
 Best Local Similarity 32.5%; Pred. No. 2e-14;
 Matches 51; Conservative 26; Mismatches 73; Indels 7; Gaps 1;

 QY 19 GLSQITKSLYISNGVAANKMLSSNQITWVINSVEVYNTLYEDIQYMQVPVADSPNSR 78
 DB 178 GPVEILPFLYLGSAHAKCEFLANLHITALLNVSRRTSEACTTHLYKWIPIVEDSHAD 237

 QY 79 LCDFFDPIADHITHSVEMKQRTLLHCAAGVSRSAALCLAYLMKYHAMSLLDHATWTKSCR 138
 DB 238 ISSHFOEAIDFIDCVREKGGKVLVHCEAGVSRSPICMAYLMKTKOFLRKEAPDYIKORR 297

 QY 139 PIIRPNSGFWEQLIHYEFOLFGKNTVMVSSPVGMIP 175
 DB 298 SMVSPNFGFMGQLQYSEI-----LPSTPTQPP 327

 RESULT 13
 DUS8_HUMAN STANDARD; PRT: 625 AA.
 ID Q13202;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (Dual specificity protein phosphatase hVH-5).
 GN DUSP8 OR VH5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=96009533; PubMed=7561881;
 RA Martell K.J., Seasholtz A.F., Kwak S.P., Clemens K.K., Dixon J.E.;
 RT "hVH-5: a protein tyrosine phosphatase abundant in brain that
 RT inactivates mitogen-activated protein kinase";
 RL J. Neurochem. 65:1823-1833(1995).
 CC -!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
 CC PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
 CC SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, HEART, AND SKELETAL MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
 CC -----
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CC	EMBL; U27193; AAA83151.1; -	
DR	HSSP; Q16828; 1MKP	
DR	Genew; HGNC:3074; DUSP8.	
DR	MM; 602038.	
DR	InterPro: IPR000340; DS_phosphatase.	
DR	InterPro: IPR001783; Rhodanese-like.	
DR	InterPro: IPR000387; TYR_phosphatase.	
DR	Pfam; PF00782; DSPC; 1.	
DR	SMART; SM00195; DSPC; 1.	
DR	SMART; SM00450; RHOD; 1.	
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.	
DR	PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.	
DR	PROSITE; PS50094; TYR_PHOSPHATASE_DUAL; 1.	
KW	Hydrolase; Nuclear protein.	
FT	DOMAIN 13 136	RHODANESE.
FT	DOMAIN 162 430	PROTEIN-TYROSINE PHOSPHATASE.
FT	DOMAIN 310 550	PRO-RICH.
FT	DOMAIN 246 246	BY SIMILARITY.
FT	ACT_SITE 245	
SQ	SEQUENCE 625 AA; 655840 MW; DCBEAL44487219666 CRC64;	

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Query Match      22.4%; Score 219.5; DB 1; Length 625;
Best Local Similarity 31.7%; Pred. No. 3.7e-14;
Matches 51; Conservative 35; Mismatches 62; Indels 13; Gaps 3;

QY 4 PCSAFPYQFPQPSYS----GLSQITKSLYTSINGVAANNKMLSSNQITMTWINSVYEVNT 59
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 141 PAALLPMSLSPCPUPVPVSGVLTIRLPHLYLQSQDXVLLNKOLMTONGISYVLNAS----NS 196

QY 60 LYE-----DQYMGVPVADSPNSLCLCFEDPIAGHHISVENKQGRTHLHCAAGYSRSAAL 114
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 197 CPKPDFICEGRFMVPPNDNYCEKLLPWLDKSIIEFDKAKLSSCOVIVHCLAGLSRSATI 256
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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QY      115 CLAYLMKYHANSLLDAHTWTKSCRPIIRNSGFEQLIHYE 155
DB      257 AIIKKTGMGSSDDAYRFVKDRRPSISPNFNLGLLEYE 297

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RESULT 14	
DUS8_MOUSE	
ID	DUS8_MOUSE
STANDARD;	PRT; 663 AA.
AC	O09112;
DT	15-JUL-1999 (Rel. 38, Created)
DT	15-JUL-1999 (Rel. 38, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16)
DE	(Neuronal tyrosine phosphatase 1).
GN	DUSP8 OR NTP1.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RC MEDLINE=96311565; PubMed=8733137;
RA Theodosiou A.M., Rodrigues N.R., Nesbitt M.A., Ambrose H.J.,
RA Paterson H., McEllellan-Arnold E., Boyd Y., Leversha M.A., Owen N.,
RA Blake D.J., Ashworth A., Davies X.E.;
RT "A member of the MAP kinase phosphatase gene family in mouse
RT containing a complex trinucleotide repeat in the coding region.";
RL Hum. Mol. Genet. 5:675-684(1996).

CC -!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
CC PHOSPHATASE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H₂O = protein
CC tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H₂O = a protein +
CC phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.

CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN AND LUNG.
CC
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC
CC -1- SIMILARITY: CONTAINS 1 RHODANSE DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).

EMBL; X95518;	CAA64772.1;	-
DR	HSP; Q16828;	IMKP.
DR	MGD; MGI:106626;	Nttp1.
DR	InterPro; IPR000340;	DS_phosphatase.
DR	InterPro; IPR001763;	Rhodanese-like.
DR	InterPro; IPR000387;	Tyr_phosphatase.
DR	Pfam; PF00782;	DSPC; 1.
DR	SMART; SM00195;	DSPC; 1.
DR	SMART; SM00450;	RHOD; 1.
DR	PROSITE; PS00383;	TYR_PHOSPHATASE_1; 1.
DR	PROSITE; PS50036;	TYR_PHOSPHATASE_2; 1.
DR	PROSITE; PS50054;	TYR_PHOSPHATASE_DUAL; 1.
KW	Hydrolase; Nuclear protein.	
FT	DOMAIN	13
FT	DOMAIN	136
FT	DOMAIN	162
FT	DOMAIN	432
FT	DOMAIN	452
FT	DOMAIN	459
FT	DOMAIN	555
FT	DOMAIN	558
FT	DOMAIN	559
FT	DOMAIN	576
FT	DOMAIN	577
FT	DOMAIN	582
FT	DOMAIN	311
FT	DOMAIN	552
FT	ACT_SITE	246
FT	ACT_SITE	246
SQ	SEQUENCE	663 AA; 69847 MW; 416F429A12C1FA7C CRC64;

Query Match	21.7%	Score	212.5;	DB	1;	Length	563;
Best local Similarity	32.9%;	Pred.	No. 2e-13;				
Matches	55;	Conservative	34;	Mismatches	59;	Indels	19;
				Gaps			5;

```

QY      2  TAPSCA-----FPVQFPROPSYSGLSOITKSYLSNGVAANKMLSSNQITWVNSVEV  56
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     143  TLPNSLSQPCLPV----PSV-GITRILPHLYLSQDKVDLNDLMTQNGISYVLNAS--  194

QY     57  VNTLYE-----DIQYMQVFVADSPNSRLCDFDPIADRIHSVEMKQGRTLHCAAGVRS  111
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    195  -NSCPKPDFICESRFRIPINDNYCEKLLPLWLDKIEFDKRAKLUSSCGVIVHCLAGISRS  253

QY    112  AALCGLAYLMKYHAKSLDLDAHTWTSCRPILIRPNSGFWEQLIHYEQL  158
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   254  ATIAIATIMKTGMSDDAYRFDVKDRRPSISPNFNFGLQLEYERSL  300

```

RESULT 15
DUSX_HUMAN
ID DUSX_HUMAN STANDARD; PRT: 665 AA.
AC Q9BY84: O9CG03;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dual specificity protein phosphatase 1? (EC 3.1.3.48) (EC 3.1.3.16)
DE (Mitogen-activated protein kinase phosphatase 7) (MAP kinase
DE phosphatase 7) (MKP-7).
GN MKP7 OR KIAA1700.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX

SEQUENCE FROM N. A.
MEDLINE=21486429; PubMed=11489891;
Masuda K., Shima H., Watanabe M., Kikuchi K.;
"MKP-7, a novel mitogen-activated protein kinase phosphatase,

functions as a shuttle protein.";
RL J. Biol. Chem. 276:39002-39011(2001).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21082932; PubMed=11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIX.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
RT DNA Res. 7:347-355(2000).
CC -!- FUNCTION: Involved in the inactivation of MAP kinases.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC -----
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CC -----
DR EMBL; AB052156; BAB40814.1; -
DR EMBL; AB051487; BAB21791.1; ALT_INIT.
DR HSP; Q16828; IMAP.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR001763; Rhodanese-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00581; Rhodanese; 2.
DR Pfam; PF00782; DSPC; 2.
DR SMART; SM00195; DSPC; 1.
DR SMART; SM00012; FPC_DSPC; 1.
DR SMART; SM00450; RHOD; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolase; Nuclear protein.
FT DOMAIN 11 131 RHODANESE.
FT DOMAIN 227 289 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 244 244 BY SIMILARITY.
SQ SEQUENCE 665 AA; 73101 MW; 1BD853FF08460DFF CRC64;

Query Match 21.3%; Score 208.5; DB 1; Length 665;
Best Local Similarity 33.8%; Pred. No. 5e-13;
Matches 54; Conservative 25; Mismatches 66; Indels 13; Gaps 3;

QY 5 SCAPVQFTQPSVS-----GLSQITSLYISNGVAANKMLSSNQITMTVINSVEVWVT- 59
DQ 140 STLVPTCISQPCLPVANIGTRILPNLYLGCQDVLNKLMOQNGIGYVLNAS----NTC 195
QY 60 ----LYEDIQYMGVPVADSPNSKLCDFDPIDAHISVEMKCGRTLLHCAAGVSRSAALC 115
DB 196 PRPDFIPESHFLRVPVNDSECEKILFWLKSVDFTIEKASNSGCVLVHCLAGISRSATIA 255
QY 116 LAYLMKYHAMSLDAHTWTKSCRPPIIRPNSGFEQLIHYE 155
DB 256 IAVIMRMDMSLDSEAYRFVKEKRPTISPNFNLGQLLDYE 295

Search completed: April 21, 2003, 18:33:12
Job time : 22 secs